1. Method of modification of the development and/or composition of cells, tissue or organs *in vivo* other than to confer trehalose synthesizing capability by inducing a change in the metabolic availability of trehalose-6-phosphate.

2. Method for the stimulation of carbon flow in the glycolytic direction in a cell by decreasing the intracellular availability of trehalose-6-phosphate.

3. Method for the inhibition of carbon flow in the glycolytic direction in a cell by increasing the intracellular availability of trehalose-6-phosphate.

4. Method for the inhibition of photosynthesis in a cell by decreasing the intracellular availability of trehalose-6-phosphate.

5. Method for the stimulation of photosynthesis in a cell by increasing the intracellular availability of trehalose-6-phosphate.

6. Method for the stimulation of sink-related activity by increasing the intracellular availability of trehalose-6-phosphate.

7. Method for the stimulation of growth of a cell or tissue by decreasing the intracellular availability of trehalose-6-phosphate.

8. Method for obtaining a dwarfed organism by increasing the intracellular availability of trehalose-6-phosphate.

9. Method for increasing metabolism of cells by decreasing the intracellular availability of trehalose-6-phosphate.

10. Method according to claim 2, 4, 7 or 9, characterized in that said decrease of the intracellular concentration of trehalose-6-phosphate is effected by an increase in trehalose-phosphate-phosphatase (TPP) activity.

11. Method according claim 10, characterized in that the increase in TPP activity is achieved by transformation of said cells with a vector capable of expression of the enzyme TPP.

12. Method according to claim 11, characterized in that said cells are transformed with a vector comprising a heterologous gene encoding TPP.

13. Method according to claim 2, 4, 7 or 9, characterized in that said decrease of the intracellular concentration of trehalose-6-phosphate is effected by a decrease in trehalose-phosphate synthase (TPS) activity.

14. Method according to claim 13, characterized in that said decrease in TPS activity is effected by transformation of said cells with a vector capable of expression of a molecule that inhibits TPS.

15. Method according to claim 14, characterized in that said vector comprises the antisense gene of TPS.

16. Method according to claim 10, characterized in that said decrease is due to mutation of the endogenous TPP enzyme.

17. Method according to claim 10, characterized in that the decrease of trehalose-6-phosphate is effected by the relative overexpression of a phospho-alpha-(1,1)-glucosidase.

18. Method according to claim 3, 5, 6 or 8, characterized in that said increase of the intracellular concentration of trehalose-6-phosphate is effected by an increase in TPS activity.

19. Method according to claim 18, characterized in that the increase in TPS activity is achieved by transformation of said cells with a vector capable of expression of the enzyme TPS.

20. Method according to claim 19, characterized in that said cells are transformed with a vector comprising a heterologous gene encoding TPS.

21. Method according to claim 3, 5, 6 or 8, characterized in that said increase of the intracellular concentration of trehalose-6-phosphate is effected by a decrease in TPP activity.

22. Method according to claim 21, characterized in that said decrease in TPP activity is effected by transformation of said cells with a vector capable of expression of a molecule that inhibits TPP.

23. Method according to claim 22, characterized in that said vector comprises the antisense gene of TPS.

24. Method according to claim 18, characterized in that said increase is due to a mutation of the endogenous TPS enzyme.

25. Method according to any one of claims 1-24, characterized in that said cell or cells are located in a plant.

26. Method according to claim 25, characterized in that said plant is a transgenic plant.

27. Method according to claim 26, characterized in that said transgenic plant is produced by transformation with *Agrobacterium tumefaciens*.

28. Method according to any one of claims 1-24, characterized in that said cell or cells are located in an animal, preferably a mammal, more preferably a human being.

29. Method according to any one of claims 1-24, characterized in that said cells are microorganisms, preferably a microorganism selected from the group consisting of bacteria, microbes, yeasts, fungi, cell cultures, oocytes, sperm cells, hybridomas, Protista and callus.

30. A cloning vector which comprises a gene coding for TPP, said gene not being a yeast TPP-gene.

31. The cloning vector of claim 30, characterized in that it comprises a nucleotide sequence selected from the group of nucleotide sequences depicted in $EQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO:17 and the parts coding for TPP from the bipartite enzymes as coded by SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 39, SEQ ID NO: 42 and SEQ ID NO: 44.

32. A cloning vector which comprises an antisense gene for TPS, which upon expression is able to prevent functional activity of the endogenous TPS gene.

33. A cloning vector which comprises a gene for TPS, characterized in that it comprises a nucleotide sequence selected from the group of nucleotide sequences depicted in SEQ ID NO: 10, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 44.

34. A cloning vector which comprises an antisense gene for TPP, which upon expression is able to prevent functional activity of the endogenous TPP gene.

35. Plant characterized in that it or one of its ancestors is transformed with a vector comprising the nucleotide sequence coding for TPP, said gene not being a yeast TPP-gene, said plant still containing said nucleotide sequence.

36. Plant characterized in that it or one of its ancestors is transformed with a vector comprising the nucleotide sequence coding for an antisense gene of TPP, said plant still containing said nucleotide sequence.

37. Plant characterized in that it or one of its ancestors is transformed with a vector comprising the nucleotide sequence coding for an antisense gene of TPS, said plant still containing said nucleotide sequence .

38. Use of trehalose-6-phosphate to influence carbohydrate partitioning in cells.

39. Use of trehalose-6-phosphate to increase biomass.

40. Use of trehalose-6-phosphate to affect *in vivo* hexokinase activity.

41. Use of trehalose-6-phosphate to affect *in vivo* hexokinase signalling function.

42. Use of trehalose-6-phosphate to affect cell wall synthesis.

43. Use of compounds influencing the intracellular availability of trehalose-6-phosphate to increase biomass.

44. Use of compounds influencing the intracellular availability of trehalose-6-phosphate to affect hexokinase activity.

45. Use of compounds influencing the intracellular availability of trehalose-6-phosphate to affect photosynthesis.

46. Use of compounds influencing the intracellular availability of trehalose-6-phosphate to affect the carbon flow in the glycolytic pathway.

47. Method for the prevention of cold sweetening by increasing the intracellular availability of trehalose-6-phosphate.

48. Method for the inhibition of invertase in beet after harvest by increasing the intracellular availability of trehalose-6-phosphate.

49. Use of compounds influencing the intracellular availability of trehalose-6-phosphate to affect cold sweetening or invertase inhibition.

50. Method according to claim 47 or 48, characterized in that increasing the intracellular availability of T-6-P results from the increase of trehalose phosphate synthase activity.

51. Method according to claim 47, characterized in that the regulation of the availability of T-6-P is specifically altered in potato tubers.

52. Method according to claim 51, characterized in that a gene coding for trehalose phosphate synthase is specifically expressed in tubers.

53. Method according to claim 52, characterized in that said gene is the TPS gene from *Escherichia coli*.

54. Method according to claim 48, characterized in that the regulation of the availability of T-6-P is specifically altered in beet taproots.

55. Method according to claim 54, characterized in that a gene coding for trehalose phosphate synthase is specifically expressed in taproots.

56. Method for the accumulation of trehalose, characterized in that an organism is transformed with a DNA sequence coding for a bipartite TPS-TPP enzyme.

57. Method according to claim 56, characterized in that said gene is the bipartite gene from *Arabidopsis thaliana*.

58. Method according to claim 56, characterized in that said gene is the bipartite gene from *Selaginella lepidophylla*.

59. Method according to claim 56, characterized in that said gene is the human bipartite gene.

60. Method according to claim 56, characterized in that said gene is the bipartite gene from *Helianthus annuus*.

61. Method to prevent metabolic steering during the production of trehalose by expression of a DNA sequence coding for a bipartite TPS-TPP enzyme.

62. Method according to claims 1-24, characterized in that expression of TPP or TPS is limited to a specific tissue.

63. Method according to claims 1-24, characterized in that expression of TPP or TPS is under control of an inducible promoter.

64. Method for the stimulation of carbon flow in the glycolytic direction in a cell by expression of trehalose-6-phosphate phosphatase.

65. Method for the inhibition of carbon flow in the glycolytic direction in a cell by expression of trehalose-6-phosphate synthase.

66. Method for the inhibition of photosynthesis in a cell by expression of trehalose-6-phosphate phosphatase.

67. Method for the stimulation of photosynthesis in a cell by expression of trehalose-6-phosphate synthase.

68. Method for the stimulation of sink-related activity by expression of trehalose-6-phosphate synthase.

69. Method for the stimulation of growth of a cell or tissue by expression of trehalose-6-phosphate phosphatase.

70. Method for obtaining organisms of reduced size by expression of trehalose-6-phosphate synthase.

71. Method for increasing metabolism of cells by expression of trehalose-6-phosphate phosphatase.

72. Method for the prevention of cold sweetening by expression of trehalose-6-phosphate synthase.

73. Method for the prevention of bolting by decreasing the intracellular availability of trehalose-6-phosphate.

74. Method for the prevention of bolting by expression of trehalose-6-phosphate phosphatase.

75. Method for the induction of bolting by increasing the intracellular availability of trehalose-6-phosphate.

76. Method for the induction of bolting by expression of trehalose-6-phosphate synthase.

77. Method for increasing the yield of plants by transforming them with an enzyme coding for trehalose-6-phosphate phosphatase.

78. Method for increasing the yield of plants by increasing the intracellular availability of trehalose-6-phosphate.

79. Polynucleotide coding for trehalose-6-phosphate synthase, characterized in that it is a bipartite enzyme which has a mutation in the part coding for trehalose-6-phosphate phosphatase.

80. Polynucleotide coding for trehalose-6-phosphate phosphatase, characterized in that it is a bipartite enzyme which has a mutation in the part coding for trehalose-6-phosphate synthase.

81. Polynucleotide according to claim 79 or 80, characterized in that the bipartite gene is human TPS/TPP.

82. Polynucleotide according to claim 81, characterized in that the human TPS/TPP has an amino acid sequence according to SEQ ID NO: 11.

83. Polynucleotide according to claim 82, characterized in that it comprises the polynucleotide sequence of SEQ ID NO:10.

84. Polynucleotide according to claim 79 or 80, characterized in that the bipartite gene is *Arabidopsis thaliana* TPS/TPP.

85. Polynucleotide according to claim 84, characterized in that the human TPS/TPP has an amino acid sequence according to SEQ ID NO: 40.

86. Polynucleotide according to claim 85, characterized in that it comprises the polynucleotide sequence of SEQ ID NO:39.

87. Polynucleotide according to claim 79 or 80, characterized in that the bipartite gene is *Selaginella lepidophylla* TPS/TPP.

88. Polynucleotide according to claim 87, characterized in that the human TPS/TPP comprises an amino acid sequence according to SEQ ID NO: 43 or a mutein thereof.

89. Polynucleotide according to claim 88, characterized in that it comprises the polynucleotide sequence of SEQ ID NO:42 or SEQ ID NO:44.

90. Polynucleotide according to claim 79 or 80, characterized in that the bipartite gene is *Helianthus annuus* TPS/TPP.

91. Polynucleotide according to claim 90, characterized in that the human TPS/TPP comprises an amino acid sequence according to SEQ ID NO: 25 or a mutein thereof.

92. Polynucleotide according to claim 91, characterized in that it comprises the polynucleotide sequence of SEQ ID NO:24 or SEQ ID NO:26 or SEQ ID NO:28.

93. Vector harbouring a polynucleotide according to any of claims 79 to 92.

94. Host organism comprising a vector according to claim 93.

95. Host organism according to claim 94, characterized in that it is *Agrobacterium tumefaciens*.

96. Cell transformed with a host organism according to claim 94 or 95.

97. Cell according to claim 96, characterized in that it is a plant cell.

98. Plant or plant part, regenerated from the plant cell according to claim 97.